

P. Gumbel

ENTERED



1600

## RAW SEQUENCE LISTING

DATE: 07/23/2002

PATENT APPLICATION: US/09/251,073A

TIME: 10:17:39

Input Set : A:\10274-003003.TXT

Output Set: N:\CRF3\07232002\I251073A.raw

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4 <110> APPLICANT: Lobb, Roy R.
5      Burkly, Linda C.
7 <120> TITLE OF INVENTION: TREATMENT FOR ASTHMA
10 <130> FILE REFERENCE: 10274-003003
12 <140> CURRENT APPLICATION NUMBER: 09/251,073A
13 <141> CURRENT FILING DATE: 1999-02-16
15 <150> PRIOR APPLICATION NUMBER: 08/822,830
16 <151> PRIOR FILING DATE: 1997-03-21
18 <150> PRIOR APPLICATION NUMBER: 08/456,193
19 <151> PRIOR FILING DATE: 1995-05-31
21 <150> PRIOR APPLICATION NUMBER: 08/374,331
22 <151> PRIOR FILING DATE: 1995-01-18
24 <150> PRIOR APPLICATION NUMBER: 08/256,631
25 <151> PRIOR FILING DATE: 1994-07-12
27 <150> PRIOR APPLICATION NUMBER: PCT/US93/00030
28 <151> PRIOR FILING DATE: 1993-01-12
30 <150> PRIOR APPLICATION NUMBER: 07/821,768
31 <151> PRIOR FILING DATE: 1992-01-13
33 <160> NUMBER OF SEQ ID NOS: 16
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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38 <211> LENGTH: 363
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
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43 <221> NAME/KEY: CDS
44 <222> LOCATION: (1)...(363)
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48 Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
49 1          5          10          15
51 tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc      96
52 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
53          20          25          30
55 tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att      144
56 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
57          35          40          45
59 gga agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc      192
60 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
61          50          55          60
63 cag gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg      240
64 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
65 65          70          75          80

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67 ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt      288
68 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
69                               85                               90                               95
71 gca gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc      336
72 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
73                               100                               105                               110
75 caa ggg acc acg gtc acc gtc tcc tca      363
76 Gln Gly Thr Thr Val Thr Val Ser Ser
77                               115                               120
80 <210> SEQ ID NO: 2
81 <211> LENGTH: 121
82 <212> TYPE: PRT
83 <213> ORGANISM: Homo sapiens
85 <400> SEQUENCE: 2
86 Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
87 1                               5                               10                               15
88 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
89                               20                               25                               30
90 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
91                               35                               40                               45
92 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
93                               50                               55                               60
94 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
95 65                               70                               75                               80
96 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
97                               85                               90                               95
98 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
99                               100                               105                               110
100 Gln Gly Thr Thr Val Thr Val Ser Ser
101                               115                               120
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104 <211> LENGTH: 318
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
108 <220> FEATURE:
109 <221> NAME/KEY: CDS
110 <222> LOCATION: (1)...(318)
112 <400> SEQUENCE: 3
113 agt att gtg atg acc cag act ccc aaa ttc ctg ctt gtt tca gca gga      48
114 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
115 1                               5                               10                               15
117 gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat      96
118 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
119                               20                               25                               30
121 gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata      144
122 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
123                               35                               40                               45
125 tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc      192
126 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

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127      50      55      60
129 agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct      240
130 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
131 65      70      75      80
133 gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac      288
134 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
135      85      90      95
137 acg ttc gga ggg ggg acc aag ctg gag atc      318
138 Thr Phe Gly Gly Thr Lys Leu Glu Ile
139      100      105
142 <210> SEQ ID NO: 4
143 <211> LENGTH: 106
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 4
148 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
149 1      5      10      15
150 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
151      20      25      30
152 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
153      35      40      45
154 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
155      50      55      60
156 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
157 65      70      75      80
158 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
159      85      90      95
160 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
161      100      105
163 <210> SEQ ID NO: 5
164 <211> LENGTH: 1347
165 <212> TYPE: DNA
166 <213> ORGANISM: Homo sapiens
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (1)...(1338)
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173 atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg      48
-----174 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
175 1      5      10      15
177 ata atg ttt gca gct tct caa gct ttt aaa atc gag acc acc cca gaa      96
178 Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
179      20      25      30
181 tct aga tat ctt gct cag att ggt gac tcc gtc tca ttg act tgc agc      144
182 Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
183      35      40      45
185 acc aca ggc tgt gag tcc cca ttt ttc tct tgg aga acc cag ata gat      192
186 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
187      50      55      60

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 189 | agt | cca | ctg | aat | ggg | aag | gtg | acg | aat | gag | ggg | acc | aca | tct | acg | ctg | 240  |
| 190 | Ser | Pro | Leu | Asn | Gly | Lys | Val | Thr | Asn | Glu | Gly | Thr | Thr | Ser | Thr | Leu |      |
| 191 | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |      |
| 193 | aca | atg | aat | cct | gtt | agt | ttt | ggg | aac | gaa | cac | tct | tac | ctg | tgc | aca | 288  |
| 194 | Thr | Met | Asn | Pro | Val | Ser | Phe | Gly | Asn | Glu | His | Ser | Tyr | Leu | Cys | Thr |      |
| 195 |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |      |
| 197 | gca | act | tgt | gaa | tct | agg | aaa | ttg | gaa | aaa | gga | atc | cag | gtg | gag | atc | 336  |
| 198 | Ala | Thr | Cys | Glu | Ser | Arg | Lys | Leu | Glu | Lys | Gly | Ile | Gln | Val | Glu | Ile |      |
| 199 |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |      |
| 201 | tac | tct | ttt | cct | aag | gat | cca | gag | att | cat | ttg | agt | ggc | cct | ctg | gag | 384  |
| 202 | Tyr | Ser | Phe | Pro | Lys | Asp | Pro | Glu | Ile | His | Leu | Ser | Gly | Pro | Leu | Glu |      |
| 203 |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |      |
| 205 | gct | ggg | aag | ccg | atc | aca | gtc | aag | tgt | tca | gtt | gct | gat | gta | tac | cca | 432  |
| 206 | Ala | Gly | Lys | Pro | Ile | Thr | Val | Lys | Cys | Ser | Val | Ala | Asp | Val | Tyr | Pro |      |
| 207 |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |      |
| 209 | ttt | gac | agg | ctg | gag | ata | gac | tta | ctg | aaa | gga | gat | cat | ctc | atg | aag | 480  |
| 210 | Phe | Asp | Arg | Leu | Glu | Ile | Asp | Leu | Leu | Lys | Gly | Asp | His | Leu | Met | Lys |      |
| 211 | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |      |
| 213 | agt | cag | gaa | ttt | ctg | gag | gat | gca | gac | agg | aag | tcc | ctg | gaa | acc | aag | 528  |
| 214 | Ser | Gln | Glu | Phe | Leu | Glu | Asp | Ala | Asp | Arg | Lys | Ser | Leu | Glu | Thr | Lys |      |
| 215 |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |      |
| 217 | agt | ttg | gaa | gta | acc | ttt | act | cct | gtc | att | gag | gat | att | gga | aaa | gtt | 576  |
| 218 | Ser | Leu | Glu | Val | Thr | Phe | Thr | Pro | Val | Ile | Glu | Asp | Ile | Gly | Lys | Val |      |
| 219 |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |      |
| 221 | ctt | gtt | tgc | cga | gct | aaa | tta | cac | att | gat | gaa | atg | gat | tct | gtg | ccc | 624  |
| 222 | Leu | Val | Cys | Arg | Ala | Lys | Leu | His | Ile | Asp | Glu | Met | Asp | Ser | Val | Pro |      |
| 223 |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| 225 | aca | gta | agg | cag | gct | gta | aaa | gaa | ttg | caa | gtc | gac | aaa | act | cac | aca | 672  |
| 226 | Thr | Val | Arg | Gln | Ala | Val | Lys | Glu | Leu | Gln | Val | Asp | Lys | Thr | His | Thr |      |
| 227 |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| 229 | tgc | cca | ccg | tgc | cca | gca | cct | gaa | ctc | ctg | ggg | gga | ccg | tca | gtc | ttc | 720  |
| 230 | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe |      |
| 231 | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| 233 | ctc | ttc | ccc | cca | aaa | ccc | aag | gac | acc | ctc | atg | atc | tcc | cgg | acc | cct | 768  |
| 234 | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro |      |
| 235 |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |     |     |     |      |
| 237 | gag | gtc | aca | tgc | gtg | gtg | gtg | gac | gtg | agc | cac | gaa | gac | cct | gag | gtc | 816  |
| 238 | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val |      |
| 239 |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |      |
| 241 | aag | ttc | aac | tgg | tac | gtg | gac | ggc | gtg | gag | gtg | cat | aat | gcc | aag | aca | 864  |
| 242 | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr |      |
| 243 |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| 245 | aag | ccg | cgg | gag | gag | cag | tac | aac | agc | acg | tac | cgg | gtg | gtc | agc | gtc | 912  |
| 246 | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val |      |
| 247 |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| 249 | ctc | acc | gtc | ctg | cac | cag | gac | tgg | ctg | aat | ggc | aag | gag | tac | aag | tgc | 960  |
| 250 | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys |      |
| 251 | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |      |
| 253 | aag | gtc | tcc | aac | aaa | gcc | ctc | cca | gcc | ccc | atc | gag | aaa | acc | atc | tcc | 1008 |

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254 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
255                               325                               330                               335
257 aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca      1056
258 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
259                               340                               345                               350
261 tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc      1104
262 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
263                               355                               360                               365
265 aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg      1152
266 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
267                               370                               375                               380
269 cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac      1200
270 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
271 385                               390                               395                               400
273 ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg      1248
274 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
275                               405                               410                               415
277 cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac      1296
278 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
279                               420                               425                               430
281 aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa      1338
282 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
283                               435                               440                               445
285 tgagtgcgg      1347
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288 <211> LENGTH: 24
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Primer
295 <400> SEQUENCE: 6
296 tcgtcgacaa aactcacaca tgcc      24
298 <210> SEQ ID NO: 7
299 <211> LENGTH: 24
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Primer
306 <400> SEQUENCE: 7
307 gtaaatgagt gcggcgccg ccaa      24
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310 <211> LENGTH: 115
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Primer
317 <400> SEQUENCE: 8
318 gcggccgcgg tccaaccacc aatctcaaag cttggtaccc gggaattcag atctgcagca      60
319 tgctcgagct ctagatatcg attccatgga tcttcacatc ccaatccgcg gccgc      115

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VERIFICATION SUMMARY

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